What is claimed is:

1. A composition comprising a substantially purified thermostable AviIII peptide, said AviIII peptide comprising a catalytic domain GH74 and a carbohydrate binding domain (CBD) III.

2. The composition of claim 1 wherein the thermostable AviIII peptide is further defined as comprising a linker and a signal sequence.

3. The composition of claim 1 or 2 wherein the GH74 catalytic domain of the thermostable AviIII peptide is further defined as having a length of about 730 to about 760 amino acids.

4. The composition of claim 1, 2, or 3 wherein the carbohydrate binding domain (CBD) III of the thermostable AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. The composition of claim 1, 2, 3, or 4 wherein the carbohydrate binding domain (CBD) III of the thermostable AviIII peptide is further defined as comprising a length of about 90 amino acids.

6. The composition of claim 3 wherein the GH74 catalytic domain is further defined as the sequence of SEQ ID NO: 3.

7. The composition of claim 4 wherein the carbohydrate binding domain (CBD) III is further defined as the sequence of SEQ ID NO: 4

8. The composition of claim 4 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the sequence of SEQ ID NO: 5.

9. The composition of claim 1 further defined as comprising a sequence of SEQ ID NO: 3 and SEQ ID NO: 4.

10. The composition of claim 1 further defined as comprising a nucleic acid sequence having about 70% sequence identity to the sequence of SEQ ID NO:2.

11. The composition of claim 1 further defined as comprising a nucleic acid sequence having about 80% sequence identity to the sequence of SEQ ID NO:2.

12. A thermostable AviIII peptide having a sequence of SEQ ID NO: 1.

13. The thermostable AviIII peptide of claim 12 further defined as having a sequence of SEQ ID NO: 2.

14. An industrial mixture suitable for degrading cellulose, such mixture comprising the thermostable AviIII polypeptide of claim 1.

15. The industrial mixture of claim 14 further defined as comprising a detergent.

16. An isolated polynucleotide molecule encoding a thermostable AviIII polypeptide, said Avi III polypeptide comprising:

a) a sequence of SEQ ID NO: 1;

b) a sequence of SEQ ID NO: 3;

c) a sequence of SEQ ID NO: 4;

d) a sequence of SEQ ID NO: 5;

e) a sequence having about 70% sequence identity with the sequence of a), b), c) or d).

17. The isolated polynucleotide molecule of claim 16 comprising a nucleic acid sequence having about 90% sequence identity to the sequence of SEQ ID NO: 2.

18. The isolated polynucleotide molecule of claim 16 comprising a nucleic acid sequence having about 80% sequence identity to the sequence of SEQ ID NO: 2.

19. The isolate polynucleotide molecule of claim 16, comprising a nucleic acid sequence having about 90% sequence identity to the nucleic acid sequence encoding the sequence of SEQ ID NO:3.

20. The isolated polynucleotide molecule of claim 16, comprising a nucleic acid sequence having about 90% sequence identity to the nucleic acid sequence encoding the sequence of SEQ ID NO:5.

21. The isolated polynucleotide molecule of claim 16, comprising a nucleic acid sequence having about 90% sequence identity to the nucleic acid sequence encoding the sequence of SEQ ID NO: 1.

22. The isolated polynucleotide molecule of claim 16, further comprising a nucleic acid sequence encoding a heterologous protein in frame with the polynucleotide molecule of claim 1.

23. The isolated polynucleotide molecule of claim 22, wherein the heterologous protein is a peptide tag.

24. The isolated polynucleotide molecule of claim 22, wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, GST, or OmpA signal sequence tag.

25. The isolated polynucleotide molecule of claim 22, wherein the heterologous protein is a substrate targeting moiety.

26. The isolated polynucleotide molecule of claim 16, operably linked to a transcriptional or translational regulatory sequence.

27. The isolated polynucleotide molecule of claim 26, wherein the transcriptional or translational regulatory sequence comprises a transcriptional promoter or enhancer.

28. An isolated polypeptide molecule comprising:

a) a sequence of SEQ ID NO: 3;

b) a sequence of SEQ ID NO: 4;

c) a sequence of SEQ ID NO: 5;

d) a sequence of SEQ ID NO: 1; or

e) a sequence of SEQ ID NO: 3, SEQ ID NO:4, and SEQ ID NO: 5; or

f) a sequence having about 70% sequence identity with the sequence of a), b), c), d), or e).

29. The polypeptide molecule of claim 28, having about 90% sequence identity with the sequence of a), b), c), d), e) or f).

30. A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemaglutinin, GST, or OmpA signal sequence tag.

34. The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37. A vector comprising the polypeptide molecule of claim 28.

38. A host cell genetically engineered to express the polypeptide moleculeof claim 28.

39. The host cell of claim 38, wherein the host cell is a plant cell.

40. The host cell of claim 38, wherein the host cell is a fungi.

41. The host cell of claim 38, wherein the host cell is a bacterial cell.

42. The host cell of claim 38, wherein the host cell is a yeast.

43. A composition comprising the polypeptide molecule of claim 28 and a carrier.

44. An isolated antibody that specifically binds to the polypeptide molecule of claim 28.

45. The antibody of claim 44, wherein the antibody is a polyclonal antibody.

46. The antibody of claim 44, wherein the antibody is a monoclonal antibody.

47. A method for producing AviIII polypeptide, the method comprising:

incubating a host cell genetically engineered to express the polynucleotide molecule of claim 28.

48. The method of claim 47, further comprising the step of:

isolating the AviIII polypeptide from the incubated host cells.

49. The method of claim 47, wherein the host cell is a plant cell.

50. The method of claim 47, wherein the host cell is a bacterial cell.

51. The method of claim 47, wherein the host cell is genetically engineered to express a selectable marker.

52. The method of claim 47, wherein the host cell further comprises a polynucleotide molecule encoding one or more polypeptide molecules selected from the glycoside hydrolase family of proteins.

53. The method of claim 52, wherein the glycoside hydrolase is a thermostable glycoside hydrolase.

54. A set of amplification primers for amplification of a polynucleotide molecule encoding a thermostable AviIII, comprising:

two or more sequences comprising 9 or more contiguous nucleic acids derived from the polynucleotide molecule of claim 28 .

55. A probe for hybridizing to a polynucleotide encoding AviIII, comprising:

a sequence of 9 or more contiguous nucleic acids derived from the polynucleotide molecule of claim 28.

56. An assay method for the detection of a polynucleotide encoding a thermostable AviIII, comprising:

amplifying a nucleic acid sequence with a set of amplification primers comprising two or more sequences of 9 or more contiguous nucleic acids derived from the polynucleotide molecule of claim 28; and

correlating the amplified nucleic acid sequence with detected polynucleotide encoding a thermostable AviIII.

57. A method for assessing the carbohydrate degradation activity of AviIII comprising:

analyzing a carbohydrate degradation in the presence of AviIII and a carbohydrate degradation in the absence of AviIII on a substrate; and

comparing the carbohydrate degradation in the presence of AviIII with the carbohydrate degradation in the absence of AviIII.

58. A method for assessing the carbohydrate degradation activity of AviIII in the presence of an agent of interest comprising:

analyzing a carbohydrate degradation in the presence of AviIII and a carbohydrate degradation in the presence of AviIII and the agent of interest on a substrate exposed; and

comparing the carbohydrate degradation in the AviIII treated substrate with the carbohydrate degradation in the AviIII treated substrate in the presence of the agent of interest.

59. The method of claim 58, wherein an increase in carbohydrate degradation activity in the presence of the agent of interest demonstrates stimulation of AviIII activity and wherein a decrease in carbohydrate degradation activity demonstrates inhibition of AviIII activity.

60. The method of claim 58, wherein the carbohydrate is cellulose.

61. The method of claim 58 wherein the agent of interest is an antibody.

62. A method for reducing cellulose in a starting material, the method comprising:

administering to the starting material an effective amount of a polypeptide molecule of claim 28.

63. The method of claim 62, further comprising administering a second polypeptide molecule selected from the glycoside hydrolase family of proteins.

64. The method of claim 62, wherein the starting material is agricultural biomass.

65. The method of claim 62, wherein the starting material is municipal solid waste.